

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2005, 21:44:35 ; Search time 223 Seconds
(without alignments)
397.337 Million cell updates/sec

Title: US-10-614-990-2

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query			Description
		Match	Length	DB	
1	1268	100.0	247	2	AAR84522 Stannioca
2	1268	100.0	247	3	Aab23264 Human sta
3	1268	100.0	247	3	Aay55750 Human sta
4	1268	100.0	247	3	Aay57166 Human cor
5	1268	100.0	247	3	Aay92901 Human sta
6	1268	100.0	247	4	Aab62473 Human sta
7	1268	100.0	247	4	Aab62690 Lng108, a
8	1268	100.0	247	5	Abb06259 Human sta
9	1268	100.0	247	6	Abp97748 Amino aci

10	1268	100.0	247	6	ABR47600	Abr47600 Breast ca
11	1268	100.0	247	6	ABG72290	Abg72290 Human Cor
12	1268	100.0	247	7	ADD48082	Add48082 Human Pro
13	1268	100.0	247	7	ADI30575	Adi30575 Human sta
14	1268	100.0	247	7	ABO84399	Abo84399 Human sta
15	1268	100.0	247	8	ADQ21382	Adq21382 Human sof
16	1231	97.1	247	7	ADD48080	Add48080 Rat Prote
17	937	73.9	276	3	AAB56848	Aab56848 Human pro
18	680.5	53.7	261	1	AAP82968	Aap82968 Corpuscle
19	662.5	52.2	256	4	AAB62474	Aab62474 Coho salm
20	628	49.5	170	3	AYY55749	Aay55749 A. austra
21	628	49.5	170	7	ADI30574	Adi30574 Australia
22	358	28.2	70	4	AAM18134	Aam18134 Peptide #
23	358	28.2	70	4	ABB37166	Abb37166 Peptide #
24	358	28.2	70	4	AAM30637	Aam30637 Peptide #
25	358	28.2	70	4	ABB31928	Abb31928 Peptide #
26	358	28.2	70	4	ABB22472	Abb22472 Protein #
27	358	28.2	70	4	AAM70300	Aam70300 Human bon
28	358	28.2	70	4	AAM57878	Aam57878 Human bra
29	358	28.2	70	4	ABG52000	Abg52000 Human liv
30	358	28.2	70	4	AAM05763	Aam05763 Peptide #
31	358	28.2	70	5	ABG39940	Abg39940 Human pep
32	354.5	28.0	296	3	AYY67926	Aay67926 Mouse sta
33	354.5	28.0	296	4	AAB61623	Aab61623 Murine st
34	354	27.9	293	2	AYY41255	Aay41255 Adipogene
35	354	27.9	293	3	AAB26872	Aab26872 Human adi
36	354	27.9	293	4	AAB93965	Aab93965 Human pro
37	354	27.9	302	3	AYY67925	Aay67925 Human sta
38	354	27.9	302	4	AAB98971	Aab98971 Human adi
39	354	27.9	302	4	AAB61621	Aab61621 Human sta
40	354	27.9	302	4	AAB31797	Aab31797 Amino aci
41	354	27.9	302	4	AAB95330	Aab95330 Human pro
42	354	27.9	302	5	ABJ05546	Abj05546 Breast ca
43	354	27.9	302	5	AAE26113	Aae26113 Human BS2
44	354	27.9	302	6	ABR47601	Abr47601 Breast ca
45	354	27.9	302	6	ADA00844	Ada00844 Human bre

ALIGNMENTS

RESULT 1

AAR84522

ID AAR84522 standard; protein; 247 AA.

XX

AC AAR84522;

XX

DT 19-APR-1996 (first entry)

XX

DE Stanniocalcin from Corpuscles of Stannius.

XX

KW stanniocalcin; Corpuscles of Stannius; hypocalcaemia; hypercalcaemia;
KW electrolyte disorder; osteoporosis; Paget's disease; treatment.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1. .33
FT /label= prepro_region
FT Protein 34. .247
FT /label= mature_stanniocalcin
XX
PN WO9524411-A1.
XX
PD 14-SEP-1995.
XX
PF 09-MAY-1994; 94WO-US005136.
XX
PR 08-MAR-1994; 94US-00208005.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Olsen H, Adams MD;
XX
DR WPI; 1995-328227/42.
DR N-PSDB; AAT02438.
XX
PT Human corpuscles of Stannius polypeptide(s) - used to treat
PT hypercalcaemia, hypocalcaemia and other electrolyte disorders.
XX
PS Claim 14; Fig 1; 41pp; English.
XX
CC Stanniocalcin, a Corpuscles of Stannius polypeptide is encoded by
CC AAT02438. Stanniocalcin functions as a hypocalcaemic agent, and can be
CC used for the treatment of e.g. electrolyte disorders which lead to renal,
CC bone and heart diseases, hypertension, hypercalcaemia and disorders due
CC to elevated bone resorption, e.g. osteoporosis and Paget's disease
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSPRKSRAAQN SAEVVRC LNSALQVGCGA FACL 60
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIA NGVTSKVFLAIRRCSTFQRM 120
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 121 IAEVQE ECYSKLNVC SIAKRNP EAITEV VQLPNHFSNRYNRLVRSLL ECDED TVSTIRD 180
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNL RGEEDSPSHIK 240
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Qy 241 RTSHESA 247
Db |||||||
Qy 241 RTSHESA 247

RESULT 2
AAB23264
ID AAB23264 standard; protein; 247 AA.
XX
AC AAB23264;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human stanniocalcin.
XX
KW Human; stanniocalcin; STC; osteogenesis; bone disease; osteoporosis;
KW mineral metabolism regulator; prophylaxis; therapy.
XX
OS Homo sapiens.
XX
PN JP2000229880-A.
XX
PD 22-AUG-2000.
XX
PF 10-FEB-1999; 99JP-00033262.
XX
PR 10-FEB-1999; 99JP-00033262.
XX
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
DR WPI; 2000-605236/58.
DR N-PSDB; AAA97594.
XX
PT An osteogenesis promotor useful in the prevention and/or treatment of
PT bone diseases such as osteoporosis.
XX
PS Example 1; Page 5-6; 6pp; Japanese.
XX
CC The invention relates to a novel osteogenesis-promoting composition which
CC contains stanniocalcin (STC) as the active component. Stanniocalcin is a
CC possible regulator of mineral metabolism. The composition is useful as a
CC prophylactic and/or therapeutic agent for bone diseases such as
CC osteoporosis. The present sequence represents human stanniocalcin which
CC was used in an exemplification of the invention
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

QY 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

QY 121 IAEVQEECYSKLNVCIAKRNPEAITEVVQLPNHFSRYYNRLVRSLLCEDDETVSTIRD 180
Db 121 IAEVQEECYSKLNVCIAKRNPEAITEVVQLPNHFSRYYNRLVRSLLCEDDETVSTIRD 180

Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYNRLVRSLL ECDED TVSTIRD 180
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNL RGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNL RGEEDSPSHIK 240
Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 3

AAY55750

ID AAY55750 standard; protein; 247 AA.

XX

AC AAY55750;

XX

DT 11-FEB-2000 (first entry)

XX

DE Human stanniocalcin polypeptide.

XX

KW Stanniocalcin-alpha polypeptide; teleocalcin; hypocalcin; hypercalcemic;
KW anti-hypercalcemic glycoprotein hormone; corpuscles of stannius; PTH;
KW parathyroid hormone; bone reabsorption; osteoporosis; gene therapy; bone;
KW electrolyte disorder; renal; heart disease; osteopetrosis; human;
KW Paget's disease; hypercalcemia.

XX

OS Homo sapiens.

XX

PN US5994103-A.

XX

PD 30-NOV-1999.

XX

PF 02-JUN-1995; 95US-00460529.

XX

PR 10-NOV-1994; 94WO-US013206.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Fleischmann RD, Olsen HS;

XX

DR WPI; 2000-038260/03.

XX

PT Isolated nucleic acids encoding human stanniocalcin-alpha useful for
PT treating electrolyte disorders which lead to renal, bone and heart
PT diseases, osteoporosis and Paget's disease.

XX

PS Disclosure; Fig 3; 21pp; English.

XX

CC The invention provides a human stanniocalcin-alpha polypeptide (also
CC called teleocalcin and hypocalcin). Stanniocalcin-alpha is an anti-
CC hypercalcemic glycoprotein hormone produced by the corpuscles of
CC stannius. It has a similar reported biological activity to that of
CC parathyroid hormone (PTH) and both these proteins exhibit dual functions
CC in mammals. They exert hypercalcemic activity due to stimulation of bone
CC reabsorption. Further PTH has a biphasic action on bone metabolism (i.e.
CC at low doses it increases bone formation and at high doses it increases

CC bone reabsorption. Accordingly, human stanniocalcin-alpha and antagonists
CC of it (under different circumstances) may be used to treat osteoporosis.
CC The DNA may be used to produce human stanniocalcin-alpha according to
CC standard recombinant DNA methodologies. The human stanniocalcin-alpha may
CC be produced either in vitro in a fermentation culture or in vivo as part
CC of a gene therapy protocol, and may be used to treat electrolyte
CC disorders which lead to renal, bone and heart diseases. Due to the
CC biphasic nature of stanniocalcin-alpha it may be used to treat
CC osteoporosis, osteopetrosis and Paget's disease. Alternatively, the
CC polypeptides may be used as antigens in the production of antibodies to
CC stanniocalcin-alpha and to assay for agonists and antagonists of its
CC activity. The antibodies and antagonists may be used to inhibit the
CC activity of stanniocalcin-alpha and may be used to treat osteoporosis and
CC hypercalcemia. The present sequence represents a human stanniocalcin

xx

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
 Best Local Similarity 100.0%; Pred. No. 9.3e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGFACL 60

Db 1 MLQNSAVLLVLVI S ASATHEAEQND SVSPRKS R VAAQNSAEV VRCLNSALQV GCGA FACL 60

Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQECCYSKLNVCSIAKRNP EAITEVVQLPNHFSNRYNRVLVRSLL ECDEDTVSTIRD 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 121 IAEVQEECYSKLNVCIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180

DB 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

QY 241 RTSHESA 247

PTSHESA

241 KISHOREA 24/

RESULT 4

AAY57166

ID AAY57166 standard; protein; 247 AA.

XX

AC AAY57166;

xx

DT 11-FEB-2000 (first entry)

xx

DE Human corpuscles of stanius polypeptide.

xx

KW Corpuscles of stanius polypeptide; calcium; inhibition; human; renal;
KW therapeutic; bone; heart disease; hypocalcemia; osteoperosis.
xx

25

US *Homo sapiens.*

2

PN US5994301-A.
XX
PD 30-NOV-1999.
XX
PF 28-APR-1995; 95US-00431117.
XX
PR 08-MAR-1994; 94US-00208005.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Adams MD, Olsen HS;
XX
DR WPI; 2000-038269/03.
DR N-PSDB; AAZ39520.
XX
PT Human corpuscles of stanius polypeptides used to inhibit calcium uptake.
XX
PS Claim 4; Fig 1A-B; 23pp; English.
XX
CC This represents a human corpuscles of stanius polypeptide, having a
CC calcium uptake inhibitory activity. The cDNA is deposited under the
CC accession number ATCC Deposit No. 75652. The polypeptide can be used in a
CC method for the treatment of a patient having need to inhibit uptake of
CC calcium. The method is also used for the therapeutic treatment of renal,
CC bone, and heart diseases, and the antagonist (may be an antibody) may be
CC used for treating hypocalcemia., and osteoperosis
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCALQVGCGAFACL 60
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 5
AAY92901
ID AAY92901 standard; protein; 247 AA.

XX
AC AAY92901;
XX
DT 26-SEP-2000 (first entry)
XX
DE Human stanniocalcin protein.
XX
KW PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation;
KW adipocyte; obesity; diabetes; hypertension; heart disease.
XX
OS Homo sapiens.
XX
PN WO200016795-A1.
XX
PD 30-MAR-2000.
XX
PF 17-SEP-1999; 99WO-JP005080.
XX
PR 17-SEP-1998; 98JP-00263004.
XX
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
PI Goto M, Tomoyasu A, Yamaguchi K, Kinosaki M, Nakagawa N;
XX
DR WPI; 2000-283445/24.
DR N-PSDB; AAA11145.
XX
PT Treating or preventing obesity, which is a risk factor for diabetes,
PT hypertension and heart disease, comprises administering an agent
PT containing stanniocalcin.
XX
PS Example 1; Page 16; 19pp; Japanese.
XX
CC This sequence represents the human stanniocalcin protein. Stanniocalcin
CC is an inhibitor of the differentiation and maturation of adipocytes. The
CC protein is used for preventing and treating obesity which is a risk
CC factor for diabetes, hypertension, and heart disease. The coding sequence
CC was isolated from IMR-90 cells
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180

CC encephalomyelitis, spinal cord diseases, mental retardation such as
CC Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as
CC muscular dystrophy, myasthenia gravis, deficiencies or disorders of
CC immune system such as Addison's disease, hemolytic anemia, rheumatoid
CC arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,
CC Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic
CC lupus erythematosus, insulin dependent diabetes mellitus, allergic
CC reactions and conditions such as asthma, for treating and/or preventing
CC organ rejection or graft-versus-host disease, hyperproliferative diseases
CC such as purpura, Gaucher's disease, cardiovascular disorders such as
CC arrhythmias, telangiectasia, vasculitis, and for treatment of disease or
CC disorders with neovascularization. The composition can be used to treat
CC hemangioma, psoriasis, angiofibroma, atherosclerotic plaques, delayed
CC wound healing, granulations, Osler-Weber syndrome, solid tumors such as
CC Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as
CC Alzheimer's disease, Parkinson's disease, wound healing, and for treating
CC or detecting infectious agents. The present sequence represents the human
CC STC polypeptide

xx

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGFACL 60
||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFLC 60

Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQECCYSKLNVCSIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| .

Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180

Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247

11 of 11

RESULT 7

AAB62690

ID AAB62690 standard; protein; 247 AA.

xx

AC AAB62690;

xx

DT 06-AUG-2001 (first entry)

xx

DE Lng108, a diagnostic marker for cancer.

xx

KW Lng108; cancer; diagnostic marker; cytotoxic; immune response; imaging.

XX
OS Homo sapiens.
XX
PN WO200132209-A1.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000; 2000WO-US030482.
XX
PR 04-NOV-1999; 99US-0163444P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Recipon H, Macina RA, Chen S, Sun Y;
XX
DR WPI; 2001-316386/33.
DR N-PSDB; AAF83823.
XX
PT Novel assay for diagnosing and monitoring cancer, involves determining
PT levels of Lng108 in cells, tissues or bodily fluids of the patient, and
PT comparing with control.
XX
PS Disclosure; Page 33-34; 36pp; English.
XX
CC The invention relates to diagnosing the presence of cancer or diagnosing
CC metastases of cancer in a patient that involves determining levels of
CC Lng108 in a sample of cells, tissues or bodily fluids in a patient, and
CC comparing the determined levels with levels of Lng108 a normal human
CC control. The method is useful for diagnosing the presence of cancer,
CC diagnosing metastases of cancer, staging cancer, monitoring cancer, and
CC monitoring a change in stage of the cancer, in a patient. A therapeutic
CC agent which is an antibody labeled with paramagnetic ions or a
CC radioisotope, and conjugated with a cytotoxic agent is useful for imaging
CC cancer in a patient. A molecule which downregulates the expression or
CC activity of Lng108, is useful for treating cancer in a patient. Lng108
CC protein is useful for inducing an immune response against a target cell
CC expressing Lng108. The present sequence represents the human Lng108
CC polypeptide
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCALQVGCGAFACL 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCALQVGCGAFACL 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 ENSTCDTGYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ENSTCDTGYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db |||||||
181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db |||||||
241 RTSHESA 247

RESULT 8

ABB06259

ID ABB06259 standard; protein; 247 AA.

XX

AC ABB06259;

XX

DT 23-MAY-2002 (first entry)

XX

DE Human staniocalcin 1 protein.

XX

KW Human; staniocalcin 1; osteopathic; osteogenesis failure; osteoporosis;
KW bone mass reduction; traumatic bone injury; osteomalacia; bone disease;
KW rheumatic bone disease; cancer associated bone disease; rachitis;
KW arthritis deformans.

XX

OS Homo sapiens.

XX

PN WO200204013-A1.

XX

PD 17-JAN-2002.

XX

PF 10-JUL-2001; 2001WO-JP005962.

XX

PR 11-JUL-2000; 2000JP-00209926.

XX

PA (BMLB-) BML INC.

XX

PI Yoshiko Y, Koide Y, Igarashi A, Takano S, Maeda N, Aubin JE;

XX

DR WPI; 2002-164600/21.

DR N-PSDB; ABL40225.

XX

PT Agent used for treating bone diseases e.g. osteoporosis, traumatic bone
PT injury, osteomalacia, rheumatic bone diseases, bone diseases associated
PT with cancer and arthritis deformans containing staniocalcin I.

XX

PS Claim 2; Fig 1; 24pp; Japanese.

XX

CC The present invention describes an agent containing staniocalcin 1,
CC particularly of human origin. Staniocalcin 1 has osteopathic activity.
CC The agent can be used for treating diseases relating to osteogenesis
CC failure or reduction in bone mass e.g. osteoporosis, traumatic bone
CC injury, osteomalacia, rheumatic bone diseases, bone diseases associated
CC with cancer, bone diseases due to phosphorus or calcium metabolic error,
CC rachitis and arthritis deformans. The agent increases bone mass. The
CC present sequence represents human staniocalcin 1

XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 5; Length 247;
 Best Local Similarity 100.0%; Pred. No. 9.3e-124;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL	60
Db	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL	60
Qy	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Db	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Qy	121	IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD	180
Db	121	IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD	180
Qy	181	SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK	240
Db	181	SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK	240
Qy	241	RTSHESA 247	
Db	241	RTSHESA 247	

RESULT 9
 ABP97748
 ID ABP97748 standard; protein; 247 AA.
 XX
 AC ABP97748;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Amino acid sequence of human STC1 polypeptide.
 XX
 KW Human; angiogenesis; wound healing; retinopathy; ischemia; inflammation;
 KW microvasculopathy; bone healing; skin inflammation; HOG3; HOG8; HOG18;
 KW follicular development; CA9; HXB; IGFBP5; HFARP; STC1; mig-6; SSR4;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2003010205-A1.
 XX
 PD 06-FEB-2003.
 XX
 PF 26-JUL-2002; 2002WO-US023786.
 XX
 PR 26-JUL-2001; 2001US-0307600P.
 PR 24-JUL-2002; 2002US-00201642.
 XX
 PA (UYDU-) UNIV DUKE MEDICAL CENT.
 XX
 PI Riggins GJ, Lal A;
 XX
 DR WPI; 2003-239423/23.

DR N-PSDB; ABZ77288.

xx

PT Inhibiting angiogenesis for treating wound healing, retinopathy, ischemia, inflammation, microvasculopathy, bone healing, skin inflammation or follicular development by providing to a subject an antisense polynucleotide.

xx

PS Claim 4; Page 61; 66pp; English.

xx

CC The present sequence is a human STC1 polypeptide. It is used in the
CC method of the invention. The specification describes a method modulating
CC angiogenesis associated with wound healing, retinopathy, ischemia,
CC inflammation, microvasculopathy, bone healing, skin inflammation or
CC follicular development. The method comprises providing to a subject HOG3,
CC HOG8, HOG18, CA9, HXB, IGFBP5, HFARP, STC1, mig-6 or SSR4. The methods,
CC antisense polynucleotides, polypeptides and antibodies are useful for
CC treating wound healing, retinopathy, ischemia, inflammation,
CC microvasculopathy, bone healing, skin inflammation or follicular
CC development, or cancer such as breast, colon or lung cancer, or
CC glioblastoma

xx

SO Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGFACL 60
|||||

Qy . 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

61 ENSTCDTGYDICKSFLYSAAKFDTQGKAFVKESLKCIAANGVTSKVFLAIRRCSTFQRM 120
121 LAVYQGEFGVSKLNGGSLNPKDNEITELVQDPLVNEVWVNPBLVQGSLILEGDPRTVTTBD 130

Db 121 IAEVQEECYSKLNVC SIAKRNPEAITEVVQLPNHFSNRYYNRLVRSI LECDEDTVSTIRD 180

Qy 181 SI.MEKIG.PN.MAS.L.F.H.I.L.O.T.D.H.C.A.O.T.H.P.B.A.D.E.N.R.B.R.T.N.E.P.O.K.I.K.V.I.L.R.N.I.R.G.E.E.D.S.P.S.H.I.K 240
Dh 181 SI.MEKIG.PN.MAS.L.F.H.I.L.O.T.D.H.C.A.O.T.H.P.B.A.D.E.N.R.B.R.T.N.E.P.O.K.I.K.V.I.L.R.N.I.R.G.E.E.D.S.P.S.H.I.K 240

Qy 241 RTSHESA 247

RESULT 10

RECEIPT
ABR47600

ID ABR47600 standard: protein: 247 AA.

xx

AC ABR47600;

xx

DT 12-JUN-2003 (first entry)

xx

DE Breast cancer associated protein sequence SEQ ID NO:441.

XX
KW Human; breast cancer; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003004989-A2.
XX
PD 16-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019669.
XX
PR 21-JUN-2001; 2001US-0299887P.
PR 27-JUN-2001; 2001US-0301572P.
PR 18-JUL-2001; 2001US-0306501P.
PR 25-SEP-2001; 2001US-0325002P.
PR 05-MAR-2002; 2002US-0362585P.
PR 14-MAY-2002; 2002US-0380391P.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;
XX
DR WPI; 2003-210381/20.
DR N-PSDB; ACC50301.
XX
PT Breast cancer diagnosis or treatment by comparing the level of expression
PT of a marker in a patient sample with that in the control non-breast
PT cancer sample.
XX
PS Claim 1; SEQ ID NO 441; 128pp; English.
XX
CC The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
CC ABR47386 to ABR47632) in a patient sample and the normal level of
CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences from
CC the present invention have cytostatic activities and can be used in gene
CC therapy. The method is useful for diagnosing and treating breast cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp://wipo.int/pub/published_pct_sequences

XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCCLNSALQVGCGAFACL 60
|||
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCCLNSALQVGCGAFACL 60

PT disease, hypercalcemia and sarcoidosis.

XX

PS Claim 13; Fig 1; 26pp; English.

XX

CC The present invention relates to the isolation of human Corpuscles of
CC Stannius protein, and the polynucleotide sequence encoding it. Human
CC Corpuscles of Stannius protein inhibits calcium uptake and reduces renal
CC excretion of phosphate. The polynucleotide sequence is useful for
CC encoding Corpuscles of Stannius protein for therapeutic purposes, e.g. in
CC the treatment of electrolyte disorders that lead to renal, bone or heart
CC disease, such as arterial hypertension, disorders due to elevated bone
CC resorption (e.g. osteoporosis and Paget's disease), and hypercalcaemia
CC (e.g. hyperparathyroidism, hypervitaminosis D), tumours that raise serum
CC calcium levels by destroying bone, sarcoidosis, hyperthyroidism, adrenal
CC insufficiency, loss of serum albumin secondary to renal diseases, or
CC excessive GI calcium absorption and elevated concentration of plasma
CC proteins. The encoded polypeptide exhibits a high degree of homology to
CC Stanniocalcin from *Anguilla australis* and from *Oncorhynchus kisutch*. The
CC present sequence represents human corpuscles of stannius protein

XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCCLNSALQVGCGAFACL 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247

||| |||

Db 241 RTSHESA 247

RESULT 12

ADD48082

ID ADD48082 standard; protein; 247 AA.

XX

AC ADD48082;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human Protein P52823, SEQ ID NO 13779.

XX

KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P52823.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 247 AA;

RESULT 13

ADI30575

ID ADI30575 standard; protein; 247 AA.

xx

AC ADI30575;

XX

DT 22-APR-2004 (first entry)

xx

DE Human stannicoalcin protein.
XX
KW human; stanniocalcin-alpha; electrolyte imbalance; hypertension;
KW hyperglycaemia; migraine; renal disease; heart disease; bone disease;
KW osteoporosis; hypoglycaemia; Paget's disease.

xx

OS *Homo sapiens.*

xx

PN US2003181663-A1.

xx

PD 25-SEP-2003.

xx

PF 18-APR-2003; 2003US-00418226.

xx

PR 10-NOV-1994; 94WO-US013206.

PR

PR 28-JUL-1999; 99US-00361736.

xx

PA (HUMA-) HUMAN GENOME SCI INC.

xx

PI Olsen HS, Fleischmann RD;

xx

DR WPI; 2003-852260/79.

xx

PT New human stanniocalcin-alpha polypeptide, useful in regulating
PT electrolyte imbalances, or for diagnosing and treating a disease
PT associated with mutated forms of stanniocalcin-alpha sequences, e.g.
PT renal disease or osteoporosis.

xx

PS Disclosure; SEQ ID NO 10; 22pp; English.

xx

CC The invention comprises the amino acid and coding sequence of a human
CC stanniocalcin-alpha protein. The DNA and protein sequences of the
CC invention are useful for regulating electrolyte imbalances to treat
CC hypertension, hyperglycaemia or migraine. The DNA and protein sequences
CC are also useful in diagnosing and treating a disease associated with
CC mutated forms of stanniocalcin-alpha sequences, such as: renal disease,
CC heart disease or bone disease (e.g. osteoporosis). The DNA and protein
CC sequences may also be used to treat hypoglycaemia or Paget's disease. The
CC present amino acid sequence represents a human stanniocalcin protein.

xx

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLSASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGFACL 60
Pb 1 MTQNSAVLLVLSASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIAANGVTSKVFLAIRRCSTFQRM 120
|||||

Qy 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240

Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRTNEPQKLKVLLRNLGEEDSPSHIK 240
Cv 241 PTSHEGAA 247

Db 241 RTSHESA 247

RESULT 14

ABO84399

ID AB084399 standard; protein; 247 AA.

xx

AC ABO84399;

xx

BT 29-JUL-2004 (first entry)

22

DE Human stanniocalcin protein.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;

KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
DR N-PSDB; ABD20997.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 6; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary

XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 4202; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 8; Length 247;
Best Local Similarity 100.0%; Pred. No. 9.3e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

Search completed: January 14, 2005, 22:14:51
Job time : 235 secs

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OM protein - protein search, using sw model

Run on: January 14, 2005, 22:10:59 ; Search time 40 Seconds
(without alignments)
409.514 Million cell updates/sec

Title: US-10-614-990-2

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1268	100.0	247	2	US-08-208-005C-2	Sequence 2, Appli
2	1268	100.0	247	2	US-09-038-597A-2	Sequence 2, Appli
3	1268	100.0	247	2	US-08-460-529B-10	Sequence 10, Appli
4	1268	100.0	247	2	US-08-431-117A-2	Sequence 2, Appli
5	1268	100.0	247	4	US-09-361-736B-10	Sequence 10, Appli
6	660.5	52.1	204	2	US-08-208-005C-5	Sequence 5, Appli
7	660.5	52.1	204	2	US-09-038-597A-5	Sequence 5, Appli
8	628	49.5	170	2	US-08-460-529B-9	Sequence 9, Appli
9	628	49.5	170	4	US-09-361-736B-9	Sequence 9, Appli
10	354.5	28.0	296	3	US-08-831-132-14	Sequence 14, Appli

11	354.5	28.0	296	3	US-09-416-150-14	Sequence 14, Appl
12	354	27.9	302	3	US-08-831-132-2	Sequence 2, Appli
13	354	27.9	302	3	US-09-416-150-2	Sequence 2, Appli
14	354	27.9	302	4	US-09-193-881-23	Sequence 23, Appl
15	354	27.9	302	4	US-09-361-736B-12	Sequence 12, Appl
16	351.5	27.7	251	4	US-09-361-736B-2	Sequence 2, Appli
17	333.5	26.3	251	2	US-08-460-529B-2	Sequence 2, Appli
18	91	7.2	901	4	US-09-828-062-8	Sequence 8, Appli
19	89.5	7.1	10182	3	US-09-134-001C-3159	Sequence 3159, Ap
20	86	6.8	500	4	US-09-198-452A-299	Sequence 299, App
21	85.5	6.7	311	4	US-09-710-279-2460	Sequence 2460, Ap
22	85.5	6.7	656	3	US-09-134-001C-4322	Sequence 4322, Ap
23	83.5	6.6	290	4	US-09-655-908-6	Sequence 6, Appli
24	83.5	6.6	290	4	US-09-655-908-8	Sequence 8, Appli
25	83.5	6.6	1027	4	US-09-762-724-8	Sequence 8, Appli
26	83.5	6.6	1029	4	US-09-762-724-6	Sequence 6, Appli
27	83	6.5	319	4	US-09-710-279-792	Sequence 792, App
28	83	6.5	319	4	US-09-710-279-2008	Sequence 2008, Ap
29	83	6.5	398	4	US-09-710-279-44	Sequence 44, Appl
30	83	6.5	398	4	US-09-710-279-1498	Sequence 1498, Ap
31	83	6.5	417	3	US-09-134-001C-3810	Sequence 3810, Ap
32	82	6.5	362	3	US-09-134-001C-4670	Sequence 4670, Ap
33	81	6.4	680	3	US-09-298-924-4	Sequence 4, Appli
34	81	6.4	720	2	US-08-840-236-1	Sequence 1, Appli
35	81	6.4	720	2	US-08-505-448A-1	Sequence 1, Appli
36	79.5	6.3	609	4	US-09-538-092-711	Sequence 711, App
37	79.5	6.3	708	1	US-08-145-681-4	Sequence 4, Appli
38	79.5	6.3	708	1	US-08-453-703-4	Sequence 4, Appli
39	79.5	6.3	708	2	US-08-456-106-4	Sequence 4, Appli
40	79.5	6.3	708	3	US-08-456-108-4	Sequence 4, Appli
41	79.5	6.3	708	3	US-09-265-577-4	Sequence 4, Appli
42	79.5	6.3	708	4	US-09-633-739-4	Sequence 4, Appli
43	79	6.2	264	4	US-09-134-000C-5831	Sequence 5831, Ap
44	78.5	6.2	1288	4	US-09-546-934-4	Sequence 4, Appli
45	78	6.2	315	3	US-09-184-964-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-08-208-005C-2

; Sequence 2, Application US/08208005C

; Patent No. 5837498

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.

; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

;
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-208-005C-2

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSI LECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSI LECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 2
US-09-038-597A-2
; Sequence 2, Application US/09038597A
; Patent No. 5877290
; GENERAL INFORMATION:

APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Corpuscles of Stannius Protein,
TITLE OF INVENTION: Stanniocalcin
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,597A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,005
FILING DATE: 8-MARCH-1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-78
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN

Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 3

US-08-460-529B-10

; Sequence 10, Application US/08460529B

; Patent No. 5994103

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.

; TITLE OF INVENTION: Human Stanniocalcin-alpha

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/460,529B

; FILING DATE: June 2, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/13206

; FILING DATE: 10 NOV 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: MULLINS, J.G.

; REGISTRATION NUMBER: 33,073

; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 247 AMINO ACIDS

; TYPE: AMINO ACID

; STRANDEDNESS:

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN

US-08-460-529B-10

Query Match 100.0%; Score 1268; DB 2; Length 247;

Best Local Similarity 100.0%; Pred. No. 1.6e-136;

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAACL 60

Db ||||||| 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQN SAEVVRCLNSALQVGCGAFACL 60
Qy 61 ENSTCDTDMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 4

US-08-431-117A-2

; Sequence 2, Application US/08431117A

; Patent No. 5994301

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.

; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/431,117A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/208,005

; FILING DATE: 8 MARCH 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-296

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-431-117A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCISIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180
||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 IAEVQEECYSKLNVCISIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240
||||||||||||||||||||||||||||||||||||||||||||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240

Qy 241 RTSHESA 247
|||||||
Db 241 RTSHESA 247

RESULT 5

US-09-361-736B-10

; Sequence 10, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D1
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human
US-09-361-736B-10

Query Match 100.0%; Score 1268; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.6e-136;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
QY 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
QY 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180
QY 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
QY 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 6

US-08-208-005C-5

; Sequence 5, Application US/08208005C

; Patent No. 5837498

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.

; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/208,005C

; FILING DATE: 8 MARCH 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-78

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-208-005C-5

Query Match 52.1%; Score 660.5; DB 2; Length 204;
Best Local Similarity 60.8%; Pred. No. 3.4e-67;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;

Qy 11 LVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVCGCAFACLENSTCDT DGM 70
|: :|| : : :: |||::| :: : ::| |||| || || ||| ||| ||| ||| ||| |||
Db 12 LVLGTAATFD TDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDT DGM 70

Qy 71 YDICKSFLYSAAKFDTQGKAFVKESLKCIA NGVTSKVFLAIRRCSTFQRMIAEVQEE CYS 130
:|||: | :|| |:||| |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 71 HDICQLFFHTAATFNTQGKTFVKE SLRCIANGVTSKV FQTIRRCGVFQRMISEVQEE CYS 130

Qy 131 KLNVC SIAKRNP EAITEVVQLPNHFSNRYNRLVRSI LECDED TVSTIRDSLMEKIGPNM 190
:||:| :|: ||||| ||||:| || |||: |:||| |||:|||:|:| |: :|||:
Db 131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLACDEETVAVV RAGLVARLGPD M 190

Qy 191 ASLFHILQTDHCAQ 204
:|| :|| || |
Db 191 ETLFQLLQNKHCPQ 204

RESULT 7

US-09-038-597A-5

; Sequence 5, Application US/09038597A
; Patent No. 5877290
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein,
; TITLE OF INVENTION: Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,597A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/208,005
FILING DATE: 8-MARCH-1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-78
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-038-597A-5

Query Match 52.1%; Score 660.5; DB 2; Length 204;
Best Local Similarity 60.8%; Pred. No. 3.4e-67;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;

Qy 11 LVISASATHEAEQNDSVSPRSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
||: :|| : : :: ||:::|| :: : ::| |||| || |||| |||||||||||||
Db 12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy 71 YDICKSFLYSAAKFDTQGKAFVKESLKCIAANGVTSKVF LAIRRCSTFQRMIAEVQEECYS 130
:|||: | :||| |:||||| ||||||:||||||||| ||||| |||||:|||||||
Db 71 HDICQLFFHTAATFNTQGKTFVKESLRCIAANGVTSKVF QTIRRCGVFQRMISEVQEECYS 130

Qy 131 KLNVCIAKRNP EAITEVVQLPNHFSNRYNRLVRSI LECDED TVSTIRDSLMEKIGPNM 190
:||:| :|: ||||| ||||:| ||| |||:| :||| |||:||:| :| | :||:|
Db 131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSI LACDEETVAVV RAGLVARLGPDM 190

Qy 191 ASLFHILQTDHCAQ 204
:|| :|| |||
Db 191 ETLFQOLLQNKHCPQ 204

RESULT 8

US-08-460-529B-9
Sequence 9, Application US/08460529B
Patent No. 5994103
GENERAL INFORMATION:
APPLICANT: OLSEN, ET AL.
TITLE OF INVENTION: Human Stanniocalcin-alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,529B
FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13206
FILING DATE: 10 NOV 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-460-529B-9

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Query Match          49.5%;  Score 628;  DB 2;  Length 170;
Best Local Similarity  66.5%;  Pred. No. 1.3e-63;
Matches 113;  Conservative 30;  Mismatches 27;  Indels 0;  Gaps 0;

Qy      28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ 87
       ||| :| :| : ::| |||| ||||| ||||:|||:|||:|||:|||: ||||| |
Db      1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNDGMHEICRSFLHGAAKFDTQ 60

Qy      88 GKAFVKESLKCIANGVTSKVFIAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 147
       || |||||||||:|||:|||:|||:|||:|||:|||:|||:|||:|||: | |
Db      61 GKTFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120

Qy      148 VVQLPNHFSNRYYNRLVRSLLLECDEDTVSTIRDSLMEKIGPNMASLFHIL 197
       | |::| | |||: | ::||| ||||| :| |: :: | | || :|
Db      121 VAQVPSQFPNRYYSTLLOSLTLCDEDTVEQVRAGLVSRLPEMGVLFOLL 170

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RESULT 9
US-09-361-736B-9
; Sequence 9, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D1
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Anguilla australis
US-09-361-736B-9

Query Match 49.5%; Score 628; DB 4; Length 170;
Best Local Similarity 66.5%; Pred. No. 1.3e-63;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

Qy 28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ 87
||| :| :| : ::| ||||| |||||:||||:||||:|||:|||: |||||
Db 1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCDGMHEICRSFLHGAAKFDTQ 60

Qy 88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCASIARKNPEAITE 147
|| |||||||:||||| |||||:|||:|||:|||:|||:|||:|||:|||:
Db 61 GKTFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120

Qy 148 VVQLPNHFSNRYYNRLVRSLLLECDEDTVSTIRDSLMEKIGPNMASLFHIL 197
| |:|: | |||: | ::||| ||||| :| |: :: | | || :|
Db 121 VAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRAGLVSRLPEMGVLFQLL 170

RESULT 10

US-08-831-132-14

; Sequence 14, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lok, Si
; APPLICANT: Buddle, Michele
; APPLICANT: Downey, William
; TITLE OF INVENTION: STANNIOCALCIN-2
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,132
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-831-132-14

Query Match 28.0%; Score 354.5; DB 3; Length 296;
Best Local Similarity 31.7%; Pred. No. 5.9e-32;
Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;

Qy 7 VLLVLVISASATHEAEQNDSVSP-----RKSRAAQNSAEVVRCLNSALQVGCGA 56
| | || : | : || : | : || : || : || : | | || |
Db 10 VTLALVF--ATLDPAQGTDSTNPEGPQDRSSQQKGRSLSLQNTAEIQHCLVNAGDVGCGV 67

Qy 57 FACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIAANGVTSKVFLAIRRCST 116
| | || :: | : | : || : || : | || || : | : | : | : |
Db 68 FECFENNNSCEIQGLHGICMTFLHNAGKFDAQGKSFIKDALRCKAHALRHKGFCISRKCPA 127

Qy 117 FQRMIAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVS 176
: | : :: | || | : || | : | | | : : : | || || |
Db 128 IREMVFQLQRECYLKHDLCSAAQENVGVIVEMIHFKDLLLHEPYVDLVNLLTCGEDVKE 187

Qy 177 TIRDLSMEKIGPNMASLFHIL-----QTDHCAQTH---PRADFNRRRTNEPQKLKV 224
: | : : : | || : | : | | || : | : |
Db 188 AVTRSVQAQCEQSWGLCSILSFCTSNIQRPPTAAPEHQPLADRAQLSRPHRDTDHHLT 247

Qy 225 LLRNLRLGEEDSPSHIK----RTSHESA 247
| : || | || | : ||
Db 248 ANRGAKGERGSKSHPNAHARGRTGGQSA 275

RESULT 11

US-09-416-150-14

; Sequence 14, Application US/09416150
; Patent No. 6171822

; GENERAL INFORMATION:

; APPLICANT: Kuestner, Rolf E.
; Conklin, Darrell C.
; Lok, Si
; Buddle, Michele
; Downey, William

; TITLE OF INVENTION: STANNILOCALCIN-2

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/416,150
FILING DATE: 11-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/831,132
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-416-150-14

RESULT 12

US-08-831-132-2

; Sequence 2, Application US/08831132
; Patent No. 6008322
; GENERAL INFORMATION:
; APPLICANT: Kuestner, Rolf E.

APPLICANT: Conklin, Darrell C.
APPLICANT: Lok, Si
APPLICANT: Buddle, Michele
APPLICANT: Downey, William
TITLE OF INVENTION: STANNIOCALCIN-2
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,132
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-831-132-2

Query Match 27.9%; Score 354; DB 3; Length 302;
Best Local Similarity 32.4%; Pred. No. 6.9e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy 9 LVLVIS-----ASATHEAE-QNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
| |::: |::: | | | :| |::: |::: |::: | | | | | | | |

Qy	61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
	: :
Pb	72 ENNSCEITRGLHGICMTEFLHNAGKEDAOGKSEIKDALCKKAHALRHREGCISRKCPAIREM 131

Qy	181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQKL-----	222
	: : : :	
Pb	192 SVVOVCOEONWGSLSGSILSECTSALIOKRPTARPEROBODPTKLSRAHHCFAHHILPERSS	251

Qy 223 KVLLRNLRGEEDSPSH 238
: | :|| | ||
Db 252 RETGRGAKGERGSKSH 267

RESULT 13

US-09-416-150-2

; Sequence 2, Application US/09416150

; Patent No. 6171822

; GENERAL INFORMATION:

; APPLICANT: Kuestner, Rolf E.
; Conklin, Darrell C.
; Lok, Si
; Buddle, Michele
; Downey, William

; TITLE OF INVENTION: STANNIOLCALCIN-2

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/416,150
; FILING DATE: 11-Oct-1999
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/831,132
; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 302 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-416-150-2

Query Match 27.9%; Score 354; DB 3; Length 302;
Best Local Similarity 32.4%; Pred. No. 6.9e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy 9 LVLVIS-----ASATHEAE-QNDSVSPRKSRAAQN SAEVVRCLNSALQVGCGAFACL 60

Db	12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRSLQNTAEIQHCLVNAGDVGCGVFECF 71
Qy	61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db	72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIDALKCKAHALRHRFGCISRKCPAIREM 131
Qy	121 IAEVQEECYSKLNVCIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180
Db	132 VSQQLQRECYLKHDLCQAQENTRVIVEMIHFKDLLLHEPYVDLVNLLTCGEEVKEAITH 191
Qy	181 SLMEKIGPNMASLFHILO-TDHCAQTHPRADFNRRRTNEPQKL----- 222
Db	192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS 251
Qy	223 KVLLRNLRGEEDSPSH 238
Db	252 RETGRGAKGERGSKSH 267

RESULT 14

US-09-193-881-23

; Sequence 23, Application US/09193881A
; Patent No. 6538119
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Klass
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; TITLE OF INVENTION: Breast
; FILE REFERENCE: 6248.US.P1
; CURRENT APPLICATION NUMBER: US/09/193,881A
; CURRENT FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-193-881-23

Query Match 27.9%; Score 354; DB 4; Length 302;
Best Local Similarity 32.4%; Pred. No. 6.9e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy	9 LVLVIS-----ASATHEAE-QNDSVSPRKSRAAQN SAEVVRLNSALQVGCGAFACL 60
Db	12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRSLQNTAEIQHCLVNAGDVGCGVFECF 71
Qy	61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db	72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIDALKCKAHALRHRFGCISRKCPAIREM 131

Qy	121	IAEVQEECYSKLNVCSIAKRNP EAITEVVQLPNHFSNRYNRLVRSLL ECDEDTVSTIRD	180
	::: :: : : : : : :		
Db	132	VSQLQRECYLKHDLC AAAQENTRVIVEMIHFKDLLLHEPYV DVLVNLLTCGEEVKEAITH	191
Qy	181	SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQL-----	222
	: : : :		
Db	192	SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS	251
Qy	223	KVLLRNLRG EEDSPSH	238
	: :		
Db	252	RETGRGAKGERGSKSH	267

RESULT 15

US-09-361-736B-12
; Sequence 12, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D1
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: human
US-09-361-736B-12

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Query Match           27.9%;  Score 354;  DB 4;  Length 302;
Best Local Similarity 32.4%;  Pred. No. 6.9e-32;
Matches 83;  Conservative 45;  Mismatches 102;  Indels 26;  Gaps 4;

Qy      9 LVLVIS-----ASATHEAE-QND SVSPRKS RVA A QNSAEVV RCLNSALQVGCGA FACL 60
        | ||::: | |: | | | : | |:: | ||::|: | | : | | | | | |
Db      12 LALVLATFDPAR GTDATNPPEGPQDRSSQQKGR LSLQNTAEI QHCLVNAGDVGCGV FECF 71

Qy      61 ENSTCD TDG MYDICKSFLYSAAKFDTQGKAFVKE SLKCIANGVTSKVFLAIRRCSTFQRM 120
        ||::|: | ::| | :|::| | || | ||::|:|:|:| | : | : | | :| : | |
Db      72 ENNSCEIRGLHGICMTFLHNAGKF DAQGKSF IKDALKCKA HALRHRFGCISRKCPAIREM 131

Qy      121 IAEVQEECYSKLN VCSIAKR NPEAITEVVQLPNHFSN RYYNRLVRSLL ECDEDTVSTIRD 180
        ::::| | || | ::|: | : | | | | : | : | | | | | | : | |
Db      132 VS QLQRECYLKHDLC AAAQENTRVIVEMIHF KDL LHEPYV DLVNLLTCGEEVKEAITH 191

Qy      181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQKL----- 222
        |: | : | | | | | | | | | | | | | | | | | | | | | | | |
Db      192 SVQVQCEQN WGS LCSILSFCTSAIQK PPTAPPERQPQV DRTKLSRAHHGEAGHHLPEPSS 251

Qy      223 KVLLRNL RGEEDSPSH 238

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Db : | : || | ||
252 RETGRGAKGERGSKSH 267

Search completed: January 14, 2005, 22:22:14
Job time : 46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2005, 22:04:00 ; Search time 40 Seconds
(without alignments)
594.139 Million cell updates/sec

Title: US-10-614-990-2

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query				Description	
	Score	Match	Length	DB	ID	
1	680.5	53.7	263	2	A54648	stanniocalcin prec
2	662.5	52.2	256	2	I51197	stanniocalcin - co
3	354	27.9	302	2	JE0357	stanniocalcin homo
4	150	11.8	40	2	B60841	teleocalcin - coho
5	149	11.8	40	2	A60841	teleocalcin - sock
6	123	9.7	33	2	S06337	teleocalcin - rain
7	102	8.0	473	2	T04799	hypothetical prote
8	94	7.4	1105	2	T18295	Ap-3 adaptor compl
9	90.5	7.1	289	2	T50776	hypothetical prote
10	90.5	7.1	783	2	T38690	probable regulator
11	89.5	7.1	1126	2	T01491	ubiquitin-protein
12	89	7.0	305	2	T08121	peroxidase (EC 1.1
13	88	6.9	473	2	T45954	hypothetical prote

14	87.5	6.9	1465	2	S45628	DNA-directed DNA p
15	86	6.8	470	2	F86526	Mg++ transporter [
16	86	6.8	470	2	H72097	mg++ transporter (
17	86	6.8	510	2	T45952	hypothetical prote
18	86	6.8	556	2	S51858	probable membrane
19	86	6.8	581	2	S58201	probable membrane
20	83	6.5	250	2	D69215	conserved hypothet
21	83	6.5	250	2	S30584	hypothetical prote
22	83	6.5	365	2	T06693	hypothetical prote
23	83	6.5	1093	2	T50652	AP-3 complex beta3
24	83	6.5	1094	2	T50651	AP3-complex beta-3
25	82.5	6.5	869	2	A88710	protein C43G2.2 [i
26	82.5	6.5	1483	2	S30015	hypothetical prote
27	82.5	6.5	1757	2	T05204	hypothetical prote
28	82.5	6.5	2335	2	T40186	probable phosphati
29	82.5	6.5	2535	2	T04824	hypothetical prote
30	82	6.5	815	2	G72209	conserved hypothet
31	82	6.5	925	2	T01384	hypothetical prote
32	81.5	6.4	463	2	T15416	hypothetical prote
33	81.5	6.4	549	2	F64640	conserved hypothet
34	81.5	6.4	708	1	TFBOL	lactotransferrin p
35	81	6.4	358	2	S76692	hypothetical prote
36	81	6.4	720	2	JC5131	glycosyltransferas
37	81	6.4	1375	2	T18961	FAB1 protein homol
38	81	6.4	4377	2	A55575	ankyrin 3, long sp
39	80	6.3	281	2	H84720	probable endonucle
40	80	6.3	509	1	VGNVPC	major envelope gly
41	80	6.3	509	2	T10395	protein gp64 - Org
42	80	6.3	985	2	T00633	Ca2+-transporting
43	80	6.3	998	2	T52581	Ca2+-transporting
44	80	6.3	1178	2	S54073	probable membrane
45	80	6.3	1188	2	T46608	zinc finger protei

ALIGNMENTS

RESULT 1

A54648

stanniocalcin precursor - Australian eel

N;Alternate names: Stannius corpuscle secretory protein

C;Species: *Anguilla australis* (Australian eel)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: A54648

R;Butkus, A.; Roche, P.J.; Fernley, R.T.; Haralambidis, J.; Penschow, J.D.; Ryan, G.B.; Trahair, J.F.; Tregear, G.W.; Coghlan, J.P.

Mol. Cell. Endocrinol. 54, 123-133, 1987

A;Title: Purification and cloning of a corpuscles of Stannius protein from *Anguilla australis*.

A;Reference number: A54648; MUID:88083961; PMID:3319739

A;Accession: A54648

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-263 <BUT>

A;Cross-references: UNIPROT:P18301

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-263/Product: stanniocalcin #status predicted <MAT>

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Query Match      53.7%;  Score 680.5;  DB 2;  Length 263;
Best Local Similarity 61.4%;  Pred. No. 3.7e-51;
Matches 124;  Conservative 41;  Mismatches 36;  Indels 1;  Gaps 1;

y      1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQNSAEVVRCALNSALQVGCGAFACL 60
b      ||: | ::| ||: :| : : :: :||| :| :| : ::| |||| |||||| |||||
1 MLRMSGILTLVL-VTAAYEQDESEPLSPRTARFSASSPSDVARCLNGALQVGCSAFACL 59

y      61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
b      :||||:||||:||:||||: ||||||||| |||||||||:||||| |||||||:||:|
60 DNSTCNDGMYEICRSFLHGAAKFDTQGKTFVKESLKCIANGITSKVFLTIRRCSSFQKM 119

y      121 IAEVQEECYSKLNVCIAKRNPAAITEEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTI RD 180
b      |:|||||:|||:||:|:| |||: ||| :| :|: | |||: |:||| |||||| :|
120 ISEVQEECYSKLDLCSVAQSNPEAMGEVAQVPSQFPNRYYSTLLQSLTCDEDTVEQVRA 179

y      181 SLMEKIGPNMASLFHILQTDHC 202
b      |: :: | | || :||| |
180 GLVSRLEPEMGVLFQLLQTKAC 201

```

RESULT 2

151197

stanniocalcin - coho salmon

C;Species: *Oncorhynchus kisutch* (coho salmon)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C;Accession: I51197

R;Wagner, G.F.; Dimattia, G.E.; Davie, J.R.; Copp, D.H.; Friesen, H.G.

Mol. Cell. Endocrinol. 90, 7-15, 1992

A;Title: Molecular cloning and cDNA sequence analysis of coho salmon stannio calcin.

A;Reference number: I51197; MUID:93246046; PMID:1363790

A:Accession: I51197

A:Status: preliminary: translated from GB/EMBL/DDBJ

A: Molecule type: mRNA

A:Residues: 1-256 <WAG>

A;Cross-references: UNIPROT:Q08264; GB:S59519; NID:g299926; PIDN:AAB26419.1; PID:g299927

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Query Match           52.2%;  Score 662.5;  DB 2;  Length 256;
Best Local Similarity 53.4%;  Pred. No. 1.3e-49;
Matches 125;  Conservative 46;  Mismatches 54;  Indels 9;  Gaps 4;

7   11 LVISASATHEAEQNDSVSPRSRVAQQNSAEVVRCLNSALQVCGAFACLENSTCDTDGM 70
8   ||: :|| : : ::-||::| :: : ::| |||| || |||| ||||||||| ||||| |
9   12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70
10

11 71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
12   :||: | :|| |:||| |||||:|||||:||||| | ||| |||||:||||| |
13 71 HDICQLFFHTAATFNTQGKTFVKECSRCCIANGVTSKVFTIRRCGVFQRMISEVQEECYS 130

14 131 KLNVCΣIAKRNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRDSLMEKIGPNM 190
15   :||:| :|: ||||| ||||:| || ||||: |:||| |||:||: :| |: :||:|
16 131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLACDEETVAVVRAGLVARLGPM 190

17 191 ASLFHILQTDHCAQTHPRADFN----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239

```


R;Wagner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.
Gen. Comp. Endocrinol. 72, 237-246, 1988
A;Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho salmon.
A;Reference number: A60841; MUID:89065334; PMID:3197944
A;Accession: B60841
A;Molecule type: protein
A;Residues: 1-40 <WAG>
A;Cross-references: UNIPROT:Q08264
C;Comment: This glycoprotein hormone from the corpuscles of Stannius regulates calcium uptake through the gills.
C;Keywords: disulfide bond; glycoprotein; hormone

Query Match 11.8%; Score 150; DB 2; Length 40;
Best Local Similarity 66.7%; Pred. No. 2e-06;
Matches 26; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 35 AAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDI 73
:: : ::| |||| || |||| ||||| |||||:||
Db 2 SSNSPSDVARCLNGALAVGCGTFACLEXSTCDTDGMHDI 40

RESULT 5
A60841
teleocalcin - sockeye salmon (fragment)
C;Species: Oncorhynchus nerka (sockeye salmon)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A60841
R;Wagner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.
Gen. Comp. Endocrinol. 72, 237-246, 1988
A;Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho salmon.
A;Reference number: A60841; MUID:89065334; PMID:3197944
A;Accession: A60841
A;Molecule type: protein
A;Residues: 1-40 <WAG>
A;Cross-references: UNIPROT:P43649
C;Comment: This glycoprotein hormone from the corpuscles of Stannius regulates calcium uptake through the gills.
C;Keywords: disulfide bond; glycoprotein; hormone

Query Match 11.8%; Score 149; DB 2; Length 40;
Best Local Similarity 76.5%; Pred. No. 2.4e-06;
Matches 26; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 40 AEVVRCCLNSALQVGCGAFACLENSTCDTDGMYDI 73
::| |||| || |||| ||||| |||||:||
Db 7 SDVARCLNGALDVGCGTFACLEXSTCDTDGMHDI 40

RESULT 6
S06337
teleocalcin - rainbow trout (fragment)
N;Alternate names: hypocalcin
C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 18-Jun-1993
C;Accession: S06337
R;Lafeber, F.P.J.G.; Hanssen, R.G.J.M.; Choy, Y.M.; Flik, G.; Herrmann-Erlee,
M.P.M.; Pang, P.K.T.; Wendelaar Bonga, S.E.
Gen. Comp. Endocrinol. 69, 19-30, 1988
A;Title: Identification of hypocalcin (teleocalcin) isolated from trout stannius
corpuscles.
A;Reference number: S06337; MUID:88196801; PMID:3360288
A;Accession: S06337
A;Molecule type: protein
A;Residues: 1-33 <LAF>
A;Note: 7-Glu was also found
C;Keywords: dimer; glycoprotein; hormone
F;29/Binding site: carbohydrate (Asn) (covalent) #status experimental

```

Query Match          9.7%;  Score 123;  DB 2;  Length 33;
Best Local Similarity  65.6%;  Pred. No. 0.00033;
Matches  21;  Conservative  5;  Mismatches  6;  Indels  0;  Gaps  0;

Qy      35 AAQNSAEVVRCI NSALQVGCGAFACLENSTCD 66
       :: : ::| |||| | | |||| ||||||| ||||| |
Ph      2 SSNSR PSDV A R C I N G A L A V G C G T E A C L E N S T C D 33

```

RESULT 7

hypothetical protein F10M23.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04799
R;Bevan, M.; Lecharny, A.; Chef dor, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.;
Mewes, H.W.; Mayer, K.F.X.; Schueler, C.
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15385
A;Accession: T04799
A;Molecule type: DNA
A;Residues: 1-473 <BEV>
A;Cross-references: UNIPROT:Q9SZ16; EMBL:AL035440
A;Experimental source: cultivar Columbia; BAC clone F10M23
C;Genetics:
A;Map position: 4
A;Introns: 24/3; 92/3; 184/3; 256/3; 308/3; 412/3
A;Note: F10M23.100

```

Query Match           8.0%;  Score 102;  DB 2;  Length 473;
Best Local Similarity 21.0%;  Pred. No. 0.5;
Matches 50;  Conservative 43;  Mismatches 67;  Indels 78;  Gaps 11;

Qy      26 SVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDT---DGMYDICKSF-LYS 80
       :| :| :||: ||::: |: | :|| | | ||| | |:
Db      50 NVYKKKVELAAKSRAELLQTLSD-----ATVELSNLTTALGEKSYIDICDMSMSLFP 100

Qy      81 AAKFDTQGKAFVKESLKCIA-----NG-- 102
       | | :|| | || | |
Db      101 LQPDKTSGT--IKEQLSAAIPALEQLWQQKEERVRAFSQDVQSQIJKICEEIAGGLNNGPH 158

Qy      103 VTSKVFLAIRRCSTFQRMIAEVQEECYSKL-----NVCSIAKRN-PEAITEV-- 148

```

Db	159	VVDETDSLKRLDDFQRKLQELQEKSDRLQKVLEFVSTVHDLCAVRLDFLSTVTEVHP	218
Qy	149	-----VQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRDSLMEKIGPNMASLFHILQT	199
Db	219	SLDEANGVQTKS-ISNETLARLAKTVTLKEDKMQRLLK--LQELATQLTDLWNLMDT	273

RESULT 8

T18295

Ap-3 adaptor complex beta3A chain - mouse

C;Species: *Mus musculus* (house mouse)

C; Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 09-Jul-2004

C;Accession: T18295

R;Feng, L.; Seymour, A.B.; Jiang, S.Y.; To, A.; Peden, A.A.; Novak, E.K.; Zhen, L.; Rusiniak, M.E.; Eicher, E.M.; Robinson, M.S.; Gorin, M.B.; Swank, R.T. *Hum. Mol. Genet.* 8, 323-330, 1999

A;Title: The beta3A subunit gene (Ap3b1) of the AP-3 adaptor complex is altered in the mouse hypopigmentation mutant pearl, a model for Hermansky-Pudlak syndrome and night blindness.

A: Reference number: Z18864: MVID: 99135912: PMID: 9931340

A:Accession: T18295

A:Status: preliminary: translated from GB/EMBL/DBT-I

A:Seaweed: preliminary
A:Molecule type: mRNA

A:Residues: 1-1105 <FFEN>

A;Cross-references: UNIPROT:Q9Z1T1; EMBL:AF103809; NID:g3885987; PID:g3885988; PTID: AAC78338_1

FIDN:ARC/0550.1

A: experimental source: strain CSN/HEO
C: Genetics:

C; Genetics:

A; Gene: Ap3b1

A; Map position: 13

Query Match 7.4%; Score 94; DB 2; Length 1105;
Best Local Similarity 21.2%; Pred. No. 6.7;
Matches 55; Conservative 40; Mismatches 104; Indels 60; Gaps 11;

Qy 61 ENSTCDTDGYD-ICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFL----- 109

Db 359 ATMSIERKGMFEPYLKSF-YVRSTDPTMIKTLKLEILTNLANEANISTLLREFOTYVRSO 417

Qy 110 -----AIRRCSTFQRMIAEVQEYCYSKLNVCIAKRNP EAITE---VVQLPNHFS 156
| |::| |::| |::| |::| |::| |::| |::| |::|
Ph 418 DKOEMANTICIGCAGT SISSEETETGECNL VGLLSNDRFLVIAESEIATKKLLOMO 472

418 DRQFAAATIQTIGRCAT---SISEFTETCFNGL-VCLLSNRDEIVVAESVVVIRKLLQMQ 473

Qy 157 NRYYNRLVRSLL-E-CDETVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRR 215
: ::| : : | || | |:: || | | : |
Db 474 PAOHGEIIRHMAKFLDSITVPVARASILWLIGEN-----CERVPKIA----- 515

Ov 216 TNEPOKLKVLLRNLRGED 234

THE INTEGRATION

516 --PDVTBKMAKSETSEDD 531

RESULT 9
T50776
hypothetical protein [imported] - Vitis vinifera
C;Species: Vitis vinifera
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: T50776
R;Matsumoto, S.; Dry, I.B.; Thomas, M.
DNA Seq. 8, 109-112, 1997
A;Title: Nucleotide sequence of grapevine (Vitis vinifera) cDNA similar to SNAP proteins.
A;Reference number: Z25233
A;Accession: T50776
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-289 <MAT>
A;Cross-references: UNIPROT:P93798; EMBL:AB001375; PIDN:BAA19246.1
A;Experimental source: strain Shiraz

RESULT 10
T38690
probable regulatory protein - fission yeast (*Schizosaccharomyces pombe*)
C;Species: *Schizosaccharomyces pombe*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C;Accession: T38690
R;Brown, D.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21805
A;Accession: T38690
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-783 <BRO>
A;Cross-references: UNIPROT:O14130; EMBL:Z99568; PIDN:CAB16735.1; GSPDB:GN00066;
SPDB:SPAC3C7.04
A;Experimental source: strain 972h-; cosmid c3C7
C;Genetics:
A;Gene: SPDB:SPAC3C7.04

A;Map position: 1

C;Superfamily: GAL4 zinc binuclear cluster homology

F;35-71/Domain: GAL4 zinc binuclear cluster homology <GL4>

Query Match 7.1%; Score 90.5; DB 2; Length 783;
Best Local Similarity 23.3%; Pred. No. 9;
Matches 56; Conservative 34; Mismatches 87; Indels 63; Gaps 12;

Qy 10 VLVISASATHEAEQNDSVSPRKSrv-----AAQNSAEVVRCLNSALQVGCGAF----- 57
Db 535 IIIMSRPVLLHKMKNAKNSPRVDRINEDCILAARHLISLVHLLQNHSQLSCYSFFDYNYT 594

Qy 58 -----ACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCI----- 99
Db 595 FSSALVVLLHCV-TEPCEED---DIAMQYAYSALDYMAEGNEAAKNCARVIRLFDAHLKG 650

Qy 100 ----ANGVTSKV-FLAIRRCSTFQRMIAEVQ-----EECYSKLNVCASIARKRNPEAITEVV 149
Db 651 ARSDGNGNTSQSGFMA-----WQRWIAEVSAKDEPEKLMSPYNKSIGGGRNSNSLTPNA 704

Qy 150 QLPNHFSNRYYNR-----LVRSLLECDEDTVSTIRDSLMEKIGPNMA---SLFHILQTD 200
Db 705 NLGADVS--FFPTDDTSFLLDHSKLDDLEKFASTLDPI--KTPDLANDSSLLNWANTD 760

RESULT 11

T01491

ubiquitin-protein ligase homolog F1707.15 - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C;Accession: T01491

R;Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li, J.; Araujo, R.; Au, M.; Brendel, V.; Buehler, E.; Conway, A.B.; Conway, A.R.; Dewar, K.; Feng, J.; Kim, C.; Kurtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.A.; Theologis, A.

submitted to the EMBL Data Library, June 1998

A;Description: *Arabidopsis thaliana* chromosome 1 BAC F1707 sequence.

A;Reference number: Z14334

A;Accession: T01491

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1126 <VYS>

A;Cross-references: UNIPROT:064605; EMBL:AC003671; NID:g2833627; PID:g3176690; GSPDB:GN00059; ATSP:F1707.15

A;Experimental source: cultivar Columbia

C;Genetics:

A;Gene: ATSP:F1707.15

A;Map position: 1

A;Introns: 118/3; 224/3; 292/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3; 1093/2

F;756-1120/Domain: ubiquitin-protein ligase homology <UBI>

Query Match 7.1%; Score 89.5; DB 2; Length 1126;
Best Local Similarity 22.1%; Pred. No. 17;
Matches 46; Conservative 39; Mismatches 76; Indels 47; Gaps 8;

Qy 14 SASATHEAEQNDSVSPRKSrvAAQNSAEVVRCLNSALQVGCGAFACLENSTCD----- 66

Db	412 SSETQKDAESELVARRK-----NCAEL---YNIFLQLP-----QSDLCNLCMLLGY 455
Qy	67 ---TDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAE 123
Db	456 EGLSDKIKYSLAGEVLKKLAAVDVTHRKFELSELASGLSSSTVRVLATLSTTQKM--- 512
Qy	124 VQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIR--- 179
Db	513 -----SQNTCSMA---GASILRVLQVLSSLTSTIDDNSVGTDKETDQEEQNIMQGLKV 562
Qy	180 --DSLMEKIGPNMASLFHILQTDHCAQT 205
Db	563 ALEPLWQELGQCIS--MTELQLDHTAAT 588

RESULT 12

T08121

peroxidase (EC 1.11.1.7) - flax (fragment)

C;Species: Linum usitatissimum (flax)

C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004

C;Accession: T08121

R;Omann, F.; Tyson, H.

submitted to the EMBL Data Library, February 1998

A;Description: cDNA sequence of a basic peroxidase (FLXPER4) in flax.

A;Reference number: Z16366

A;Accession: T08121

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-305 <OMA>

A;Cross-references: UNIPROT:O65029; EMBL:AF049881; NID:g2944416;

PIDN: AAC05277.1; PID:g2944417

A;Experimental source: cv. Stormont Cirrus

C;Genetics:

A;Gene: PER4

C;Superfamily: peroxidase

C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase

F;23-103/Disulfide bonds: #status predicted

F;50/Active site: Arg #status predicted

F;54,181/Binding site: heme iron (His) (axial ligands) #status predicted

F;56-61/Disulfide bonds: #status predicted

F;109-301/Disulfide bonds: #status predicted

F;188-213/Disulfide bonds: #status predicted

Query Match 7.0%; Score 89; DB 2; Length 305;
 Best Local Similarity 21.9%; Pred. No. 3.9;
 Matches 57; Conservative 39; Mismatches 92; Indels 72; Gaps 15;

Qy	11 LVISASATHEAEQNDSVSPRSRVAAQNSAEVVRLNSALQVGCGA-FACLE-NSTCDTD 68
Db	65 LLLDDTATFTGEKN--AGPNQNSV--RGFDIIDTIKTRVEAACNATVSCADILALAARD 119
Qy	69 GMYDI-----CKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLA----- 110
Db	120 GVVLVGGPTWTVPPLGRRDARTASQSAANAQIPAPG--SSLGTITNLFTNKGLTARDVTI 176
Qy	111 -----IRR CSTFQRMIAEVQEECYSKLNV---CSI AKRN-PEA-----ITEVVQLP 152

Db	177 LSGAHTIGQARCTTFRQRI-----YNDTNIDPAFATTRRGNCQAGAGANLAPLDGTP	229
Qy	153 NHFSNRYYNRLV--RSLLCDEDVTST-IRDSDLMEKIGPNMASLFHILQTDHCAQ-----	204
Db	230 TQFDNRYYQDLVARRGLLHSDQELFNNGTQDALVRTYSNNAAT---FATDFAAMVRMG	285
Qy	205 -----THPRADFNRRRTN 217	
Db	286 NISPLTGTNGEIRFNCRPN 305	

RESULT 13

T45954

hypothetical protein F7J8.120 - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 C;Accession: T45954
 R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, January 2000
 A;Reference number: Z23018
 A;Accession: T45954
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-473 <BEV>
 A;Cross-references: UNIPROT:Q9LFC2; EMBL:AL137189
 A;Experimental source: cultivar Columbia; BAC clone F7J8
 C;Genetics:
 A;Map position: 5
 A;Introns: 29/1; 428/3
 A;Note: F7J8.120
 C;Superfamily: *Arabidopsis thaliana* hypothetical protein F7J8.130

Query Match 6.9%; Score 88; DB 2; Length 473;
 Best Local Similarity 22.6%; Pred. No. 8.1;
 Matches 54; Conservative 42; Mismatches 103; Indels 40; Gaps 13;

Qy	27 VSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLEN--STCD---TDGMYDICKS-FLY	79
Db	16 IDEEKNKVVLAEAGTIVRLLAKHRKSDPVTIGCLRNLYTSVVDMELEDDFETDACKQMLLY	75
Qy	80 SAAKFDTQGKAF-----VKESLKCIAANGVTSKVFLAIRRCSTFQRMIAE---VQEEC--	128
Db	76 PKNIREAQYRNFKLNIDTNESLKCFG---CRFFSICRMCSNFNTSLCKCGKLMNEEISF	131
Qy	129 --YSKLNVCIAKRNPEA--ITEVVQLPNHFSNRYNRLVRSLLCDEDVTSTIRDSIME	184
Db	132 LEYEENDVEGVFMRDKSSFIITDDLRLTDDST---SSLLQTLKDLGCADVSKLREQVLD	187
Qy	185 KIGPNMASLFHILQTDHCAQTH--PRAD--FNRRRTNEPQKLKVLLRNLRGEEDSPSHI	239
Db	188 -IG-----LKEVMTLMQCVFTSNTPLTDAFLKNQSSNTVRKIYRKLSDDKGDEAEPDKV	240

RESULT 14

S45628

DNA-directed DNA polymerase (EC 2.7.7.7) alpha 180K chain - mouse
N;Alternate names: DNA polymerase alpha/DNA primase complex 180K chain
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S45628; A46642
R;Stadlbauer, F.; Brueckner, A.; Rehfuss, C.; Eckerskorn, C.; Lottspeich, F.;
Foerster, V.; Tseng, B.Y.; Nasheuer, H.P.
Eur. J. Biochem. 222, 781-793, 1994
A;Title: DNA replication in vitro by recombinant DNA-polymerase-alpha-primase.
A;Reference number: S45628; MUID:94298818; PMID:8026492
A;Accession: S45628
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1465 <STA>
A;Cross-references: UNIPROT:P33609; EMBL:D17384; NID:g397829; PIDN:BAA04202.1;
PID:g442471
R;Miyazawa, H.; Izumi, M.; Tada, S.; Takada, R.; Masutani, M.; Ui, M.; Hanaoka, F.
J. Biol. Chem. 268, 8111-8122, 1993
A;Title: Molecular cloning of the cDNAs for the four subunits of mouse DNA
polymerase alpha-primase complex and their gene expression during cell
proliferation and the cell cycle.
A;Reference number: A46642; MUID:93216788; PMID:8463324
A;Accession: A46642
A;Status: preliminary.
A;Molecule type: mRNA; protein
A;Residues: 4-1465 <MIY>
A;Experimental source: FM3A cells
A;Note: sequence extracted from NCBI backbone (NCBIN:129146, NCBIPI:129147)
C;Superfamily: DNA polymerase
C;Keywords: DNA binding; nucleotidyltransferase; nucleus

Query Match 6.9%; Score 87.5; DB 2; Length 1465;
Best Local Similarity 20.7%; Pred. No. 34;
Matches 34; Conservative 32; Mismatches 55; Indels 43; Gaps 7;

Qy 6 AVLLVLVISASAT-----HEAEQNDSVSPRKSRSVAAQNSAEVVRLNSALQVGCGAFA 58
| ||: | : :| |: |:||:: : : : : | |
Db 1236 AVLIALWLGLDSTQFRVHQYHKDEENDALLGGPAQLTDEEKYK-----DCEKFK 1284

Qy 59 CLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT-----SKVFLAIR 112
| | | | : :|| :: : | : : : | : : | : : | : : ||
Db 1285 CLCPS-CGTENIYD---NVFEGSGLDMEPSLYRCNSVDCKVSPLTVMQQLSNKLIIMDIR 1339

Qy 113 RCSTFQRMIAEVQEECYSKLNVCIAKRNPAAITEVVQLPNHFS 156
| | : | : | : | : : : || ||
Db 1340 RCI-----KKYYDGWLIC---EEPTCCSRLRRPLPLHFS 1369

RESULT 15
F86526
Mg++ transporter [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86526
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.;
Shiba, T.; Ishii, K.; Hattori, M.; Kuhara, S.; Nakazawa, T.

Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: F86526
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-470 <STO>
A;Cross-references: UNIPROT:Q9Z8Q2; GB:BA000008; NID:g8978660; PIDN:BAA98496.1;
GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics:
A;Gene: mgtE
C;Superfamily: magnesium transport protein mgtE

Query Match 6.8%; Score 86; DB 2; Length 470;
Best Local Similarity 22.9%; Pred. No. 12;
Matches 47; Conservative 33; Mismatches 61; Indels 64; Gaps 13;

Qy 56 AFACLENSTCDTD-GMYDICK-----SFLYSAAKFDTQGKAFVKESELKCIANGVTSK 106
|| || || :|| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 19 AFTCL-----STDIHSHDLSKIVIEYNPIDLAYAVSCLPSESRAILYKNLSCI----TAK 69

Qy 107 VFLAIR-----RCSTFQRMIAEVQEECYSKLNVCIAKRNP--EAITEVVQLPNHFSNRY 159
| | | : | : | | ||:: :: | | | : : | : |
Pb 70 VAETINTDSASPRWATERPI-----SDSEVCALEOMPDPDEAVWVLDTP---DRP 116

Qy	208	RADFNRRRTNEPQKLKVLLRNLRG	232
		: : :	
Pb	172	GIDLTR-----LVFVLDFKGE	187

Search completed: January 14, 2005, 22:21:27
Job time : 52 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2005, 22:18:31 ; Search time 149 Seconds
(without alignments)
598.916 Million cell updates/sec

Title: US-10-614-990-2
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1268	100.0	247	9	US-09-840-989A-2	Sequence 2, Appli
2	1268	100.0	247	9	US-09-361-736-10	Sequence 10, Appl
3	1268	100.0	247	13	US-10-116-051-2	Sequence 2, Appli
4	1268	100.0	247	14	US-10-177-293-441	Sequence 441, App
5	1268	100.0	247	14	US-10-418-226-10	Sequence 10, Appl
6	1268	100.0	247	14	US-10-465-572-18	Sequence 18, Appli
7	1268	100.0	247	15	US-10-372-683-41	Sequence 41, Appli
8	1268	100.0	247	17	US-10-614-990-2	Sequence 2, Appli
9	1268	100.0	247	17	US-10-723-860-4202	Sequence 4202, Ap
10	937	73.9	276	9	US-09-925-300-1426	Sequence 1426, Ap
11	662.5	52.2	256	9	US-09-840-989A-3	Sequence 3, Appli
12	662.5	52.2	256	17	US-10-614-990-3	Sequence 3, Appli
13	660.5	52.1	204	13	US-10-116-051-10	Sequence 10, Appl
14	628	49.5	170	9	US-09-361-736-9	Sequence 9, Appli
15	628	49.5	170	14	US-10-418-226-9	Sequence 9, Appli
16	358	28.2	70	9	US-09-864-761-37770	Sequence 37770, A
17	354	27.9	302	9	US-09-193-881-23	Sequence 23, Appl
18	354	27.9	302	14	US-10-177-293-443	Sequence 443, App
19	354	27.9	302	14	US-10-338-395-23	Sequence 23, Appli
20	354	27.9	302	14	US-10-418-226-12	Sequence 12, Appli
21	354	27.9	302	14	US-10-364-889-4	Sequence 4, Appli
22	354	27.9	302	14	US-10-295-027-100	Sequence 100, App
23	354	27.9	302	15	US-10-173-999-80	Sequence 80, Appli
24	354	27.9	302	15	US-10-058-270A-22	Sequence 22, Appli
25	354	27.9	302	17	US-10-789-378-74	Sequence 74, Appli
26	351.5	27.7	251	14	US-10-418-226-2	Sequence 2, Appli
27	333.5	26.3	251	9	US-09-361-736-2	Sequence 2, Appli
28	303	23.9	118	13	US-10-116-051-9	Sequence 9, Appli
29	95.5	7.5	299	15	US-10-282-122A-49895	Sequence 49895, A
30	94.5	7.5	415	17	US-10-425-115-320042	Sequence 320042,
31	92	7.3	1010	17	US-10-425-115-312927	Sequence 312927,
32	91	7.2	901	10	US-09-828-062-8	Sequence 8, Appli
33	91	7.2	901	16	US-10-768-511-8	Sequence 8, Appli
34	90.5	7.1	783	15	US-10-149-310-96	Sequence 96, Appli
35	90	7.1	281	11	US-09-973-278-172	Sequence 172, App
36	90	7.1	281	11	US-09-973-278-277	Sequence 277, App
37	90	7.1	331	15	US-10-264-049-2324	Sequence 2324, Ap
38	89.5	7.1	622	16	US-10-437-963-161551	Sequence 161551,
39	89.5	7.1	1123	15	US-10-282-122A-70581	Sequence 70581, A
40	89.5	7.1	10203	16	US-10-661-809-23	Sequence 23, Appli
41	89	7.0	201	17	US-10-425-115-320050	Sequence 320050,
42	89	7.0	431	17	US-10-425-115-285165	Sequence 285165,
43	86	6.8	401	15	US-10-425-114-63193	Sequence 63193, A
44	86	6.8	470	15	US-10-282-122A-54827	Sequence 54827, A
45	86	6.8	500	15	US-10-289-762-299	Sequence 299, App

ALIGNMENTS

RESULT 1
 US-09-840-989A-2
 ; Sequence 2, Application US/09840989A
 ; Patent No. US20020042372A1

; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods
Based Thereon
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-989A-2

Query Match 100.0%; Score 1268; DB 9; Length 247;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDVSPrksrvaaQNSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDVSPrksrvaaQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKEsLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKEsLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCsIAKRNP EAITEVVQLPNHFSNRYNRLVRSLLECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCsIAKRNP EAITEVVQLPNHFSNRYNRLVRSLLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 2
US-09-361-736-10
; Sequence 10, Application US/09361736
; Patent No. US20020102634A1
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human Stanniocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND

;
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/361,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460,529
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-361-736-10

Query Match 100.0%; Score 1268; DB 9; Length 247;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 3

US-10-116-051-2

; Sequence 2, Application US/10116051
; Publication No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOPROTEIN
; FILE REFERENCE: PF108P1D1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-116-051-2

Query Match 100.0%; Score 1268; DB 13; Length 247;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL	60
Db	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL	60
Qy	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Db	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Qy	121	IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD	180
Db	121	IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD	180
Qy	181	SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK	240
Db	181	SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK	240
Qy	241	RTSHESA 247	
Db	241	RTSHESA 247	

RESULT 4

US-10-177-293-441
; Sequence 441, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula

; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION,
ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 441
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-441

Query Match 100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFRAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFRAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
|||
Qy 241 RTSHESA 247
|||
Db 241 RTSHESA 247

RESULT 5

US-10-418-226-10

; Sequence 10, Application US/10418226
; Publication No. US20030181663A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D2
; CURRENT APPLICATION NUMBER: US/10/418,226
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 09/361,736
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human

US-10-418-226-10

Query Match 100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
|||
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFRAIRRCSTFQRM 120
|||
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFRAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180
|||
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
|||
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
|||
Db 241 RTSHESA 247

RESULT 6
US-10-465-572-18
; Sequence 18, Application US/10465572
; Publication No. US20030207840A1
; GENERAL INFORMATION:
; APPLICANT: Riggins, Gregory
; APPLICANT: Lal, Anita
; TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
; FILE REFERENCE: 000250.00012
; CURRENT APPLICATION NUMBER: US/10/465,572
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/10/201,642
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/307,600
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-465-572-18

Query Match 100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 7
US-10-372-683-41
; Sequence 41, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PEALE JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA

; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 41
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-372-683-41

Query Match 100.0%; Score 1268; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCNSALQVGCGAFACL	60
Db	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCNSALQVGCGAFACL	60
Qy	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Db	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Qy	121	IAEVQEECYSKLNVCIAKRNPAAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD	180
Db	121	IAEVQEECYSKLNVCIAKRNPAAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD	180
Qy	181	SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK	240
Db	181	SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK	240
Qy	241	RTSHESA 247	
Db	241	RTSHESA 247	

RESULT 8

US-10-614-990-2
; Sequence 2, Application US/10614990
; Publication No. US20040198658A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods
Based Thereon
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/10/614,990
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/840,989A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-614-990-2

Query Match 100.0%; Score 1268; DB 17; Length 247;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDED TVSTIRD 180
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDED TVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 9
US-10-723-860-4202
; Sequence 4202, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions
&
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4202
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-4202

Query Match 100.0%; Score 1268; DB 17; Length 247;

Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 10

US-09-925-300-1426
; Sequence 1426, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1426
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (43)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (273)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (275)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1426

Query Match 73.9%; Score 937; DB 9; Length 276;
 Best Local Similarity 99.5%; Pred. No. 6.8e-87;
 Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL	60
Db	89	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL	148
Qy	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Db	149	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	208
Qy	121	IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD	180
Db	209	IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD	268
Qy	181	SLMEKI 186	
Db	269	SLMEXI 274	

RESULT 11

US-09-840-989A-3

; Sequence 3, Application US/09840989A
 ; Patent No. US20020042372A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olsen et al.
 ; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods
 Based Thereon
 ; FILE REFERENCE: PF108P2
 ; CURRENT APPLICATION NUMBER: US/09/840,989A
 ; CURRENT FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: PCT/US00/29432
 ; PRIOR FILING DATE: 2000-10-26
 ; PRIOR APPLICATION NUMBER: US 60/161,740
 ; PRIOR FILING DATE: 1999-10-27
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Oncorhynchus kisutch

US-09-840-989A-3

Query Match 52.2%; Score 662.5; DB 9; Length 256;
 Best Local Similarity 53.4%; Pred. No. 6.1e-59;
 Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

Qy	11	LVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACLENSTCDTDGM	70
	: : : : : :: : : :		
Db	12	LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM	70
	: : :		
Qy	71	YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS	130
	: : :		
Db	71	HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFTIRRCGVFQRMISEVQEECYS	130
	: :		
Qy	131	KLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRDLSMEKIGPNM	190

; Publication No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIocalcIN
; FILE REFERENCE: PF108P1D1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-10-116-051-10

Query Match 52.1%; Score 660.5; DB 13; Length 204;
Best Local Similarity 60.8%; Pred. No. 7.1e-59;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;

Qy 11 LVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGGAFACLENSTCDTDGM 70
||: :|| : : :: ||:::| :: : ::| |||| || |||| |||||||||||||
Db 12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy 71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
:|||: | :||| | :||| | :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVQTIIRRCGVFQRMISEVQEECYS 130

Qy 131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSILLECDEDTVSTIRDSIIMEKIGPNM 190
:||:| :|: | :||| | :|||:| | :|||:| :|||:| :|||:| :| | :|||:|
Db 131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLACDEETVAVVRAGLVARLGPDM 190

Qy 191 ASLFHILQTDHCAQ 204
:|| :|| | | |
Db 191 ETLFQOLLQNKHCPQ 204

RESULT 14
US-09-361-736-9
; Sequence 9, Application US/09361736
; Patent No. US20020102634A1
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human StanniocalcIN-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA

; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/361,736
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460,529
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN

US-09-361-736-9

Query Match 49.5%; Score 628; DB 9; Length 170;
Best Local Similarity 66.5%; Pred. No. 1.1e-55;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

Qy	28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ	87
	: : : :: : : : : :	
Db	1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNDGMHEICRSFLHGAAKFDTQ	60
	: : : : : : :	
Qy	88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCASIARKRNPEAITE	147
	: : : : : : : : : :	
Db	61 GKTGVKESLKCIANGITSKVFTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE	120
	: : : : : : : : : : : :	
Qy	148 VVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRDSLMEKIGPNMASLFHIL	197
	: : : : : : : : : : : : :	
Db	121 VAQVPSQFPNRYYSTLLQSLTCDEDTVEQVRAGLVSRLPEMGVLFQLL	170

RESULT 15

US-10-418-226-9

; Sequence 9, Application US/10418226
; Publication No. US20030181663A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stanniocalcin-Alpha
; FILE REFERENCE: PF143P1D2
; CURRENT APPLICATION NUMBER: US/10/418,226
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 09/361,736

; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Anguilla australis
US-10-418-226-9

Query Match 49.5%; Score 628; DB 14; Length 170;
Best Local Similarity 66.5%; Pred. No. 1.1e-55;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

Qy	28	SPRKSRAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ	87
	: : : :: : : : : :		
Db	1	SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNDGMHEICRSFLHGAAKFDTQ	60
Qy	88	GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCASIAGRNPAAITE	147
	: : : : : : : :		
Db	61	GKTFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE	120
Qy	148	VVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRDSLMEKIGPNMASLFHIL	197
	: : : :: : : :: :		
Db	121	VAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRAGLVSRLPEMGVLFQLL	170

Search completed: January 14, 2005, 22:33:21
Job time : 153 secs